

Claims

What is claimed is:

- 5 1. An isolated polynucleotide selected from the group consisting of:
 - a) a polynucleotide comprising SEQ ID NO: 1;
 - b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 1
over the entire length of SEQ ID NO: 1;
 - c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 1
10 over the entire length of SEQ ID NO: 1;
 - d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 1
over the entire length of SEQ ID NO: 1;
 - e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 1
over the entire length of SEQ ID NO: 1;
 - 15 f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 1 or a fragment thereof; and
 - g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).
- 20 2. An isolated polynucleotide selected from the group consisting of:
 - a) a polynucleotide comprising SEQ ID NO: 2;
 - b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 2
over the entire length of SEQ ID NO: 2;
 - c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 2
25 over the entire length of SEQ ID NO: 2;

d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 2
over the entire length of SEQ ID NO: 2;

e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 2
over the entire length of SEQ ID NO: 2;

5 f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 2 or a fragment thereof; and

g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).

10 3. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising SEQ ID NO: 3;

b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 3
over the entire length of SEQ ID NO: 3;

c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 3
15 over the entire length of SEQ ID NO: 3;

d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 3
over the entire length of SEQ ID NO: 3;

e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 3
over the entire length of SEQ ID NO: 3;

20 f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 3 or a fragment thereof; and

g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).

25 4. An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising SEQ ID NO: 4;
- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 4
over the entire length of SEQ ID NO: 4;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 4
5 over the entire length of SEQ ID NO: 4;
- d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 4
over the entire length of SEQ ID NO: 4;
- e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 4
over the entire length of SEQ ID NO: 4;
- 10 f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 4 or a fragment thereof; and
- g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).

- 15 5. An isolated polynucleotide selected from the group consisting of:
 - a) a polynucleotide comprising SEQ ID NO: 5;
 - b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 5
over the entire length of SEQ ID NO: 5;
 - c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 5
20 over the entire length of SEQ ID NO: 5;
 - d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 5
over the entire length of SEQ ID NO: 5;
 - e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 5
over the entire length of SEQ ID NO: 5;

f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID NO: 5 or a fragment thereof; and

g) a polynucleotide sequence complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), or (f).

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6. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising SEQ ID NO: 6;

b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 6 over the entire length of SEQ ID NO: 6;

10 c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 6 over the entire length of SEQ ID NO: 6;

d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 6 over the entire length of SEQ ID NO: 6;

15 e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 6 over the entire length of SEQ ID NO: 6;

f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID NO: 6 or a fragment thereof; and

g) a polynucleotide sequence complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), or (f).

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7. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising SEQ ID NO: 7;

b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 7 over the entire length of SEQ ID NO: 7;

- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 7
over the entire length of SEQ ID NO: 7;
- d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 7
over the entire length of SEQ ID NO: 7;
- 5 e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 7
over the entire length of SEQ ID NO: 7;
- f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 7 or a fragment thereof; and
- g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
10 (b), (c), (d), (e), or (f).

8. An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising SEQ ID NO: 8;
- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 8
15 over the entire length of SEQ ID NO: 8;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 8
over the entire length of SEQ ID NO: 8;
- d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 8
over the entire length of SEQ ID NO: 8;
- 20 e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 8
over the entire length of SEQ ID NO: 8;
- f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 8 or a fragment thereof; and
- g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
25 (b), (c), (d), (e), or (f).

9. An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising SEQ ID NO: 23;
- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 23
5 over the entire length of SEQ ID NO: 23;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 23
over the entire length of SEQ ID NO: 23;
- d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 23
over the entire length of SEQ ID NO: 23;
- 10 e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 23
over the entire length of SEQ ID NO: 23;
- f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 23 or a fragment thereof; and
- g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
15 (b), (c), (d), (e), or (f).

10. An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising SEQ ID NO: 24;
- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 24
20 over the entire length of SEQ ID NO: 24;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 24
over the entire length of SEQ ID NO: 24;
- d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 24
over the entire length of SEQ ID NO: 24;

e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 24
over the entire length of SEQ ID NO: 24;

f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 24 or a fragment thereof; and

5 g) a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).

11. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising SEQ ID NO: 25;

10 b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 25
over the entire length of SEQ ID NO: 25;

c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 25
over the entire length of SEQ ID NO: 25;

d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 25
15 over the entire length of SEQ ID NO: 25;

e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 25
over the entire length of SEQ ID NO: 25;

f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
NO: 25 or a fragment thereof; and

20 a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).

12. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising SEQ ID NO: 26;

- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 26 over the entire length of SEQ ID NO: 26;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 26 over the entire length of SEQ ID NO: 26;
- 5 d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 26 over the entire length of SEQ ID NO: 26;
- e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 26 over the entire length of SEQ ID NO: 26;
- f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
- 10 NO: 26 or a fragment thereof; and
- a polynucleotide sequence complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), or (f).

13. An isolated polynucleotide selected from the group consisting of:

- 15 a) a polynucleotide comprising SEQ ID NO: 27;
- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 27 over the entire length of SEQ ID NO: 27;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 27 over the entire length of SEQ ID NO: 27;
- 20 d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 27 over the entire length of SEQ ID NO: 27;
- e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 27 over the entire length of SEQ ID NO: 27;
- f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
- 25 NO: 27 or a fragment thereof; and

a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).

14. An isolated polynucleotide selected from the group consisting of:

- 5 a) a polynucleotide comprising SEQ ID NO: 28;
- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 28
over the entire length of SEQ ID NO: 28;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 28
over the entire length of SEQ ID NO: 28;
- 10 d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 28
over the entire length of SEQ ID NO: 28;
- e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 28
over the entire length of SEQ ID NO: 28;
- f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID
15 NO: 28 or a fragment thereof; and
a polynucleotide sequence complementary to the polynucleotide sequence of (a),
(b), (c), (d), (e), or (f).

15. An isolated polynucleotide selected from the group consisting of:

- 20 a) a polynucleotide comprising SEQ ID NO: 29;
- b) a polynucleotide sequence having at least 70% identity to that of SEQ ID NO: 29
over the entire length of SEQ ID NO: 29;
- c) a polynucleotide sequence having at least 80% identity to that of SEQ ID NO: 29
over the entire length of SEQ ID NO: 29;

- d) a polynucleotide sequence having at least 90% identity to that of SEQ ID NO: 29 over the entire length of SEQ ID NO: 29;
- e) a polynucleotide sequence having at least 95% identity to that of SEQ ID NO: 29 over the entire length of SEQ ID NO: 29;
- 5 f) an polynucleotide sequence that hybridizes, under stringent conditions, to SEQ ID NO: 29 or a fragment thereof; and
- a polynucleotide sequence complementary to the polynucleotide sequence of (a), (b), (c), (d), (e), or (f).

10 16. An intron obtained from a genomic polynucleotide sequence selected from the group consisting of:

- a) a genomic polynucleotide sequence having at least 70% identity to coding regions of SEQ ID NO: 1 over the entire coding regions of SEQ ID NO:1;
- b) a genomic polynucleotide sequence having at least 80% identity to coding regions of SEQ ID NO: 1 over the entire coding regions of SEQ ID NO:1;
- 15 c) a genomic polynucleotide sequence having at least 90% identity to coding regions of SEQ ID NO: 1 over the entire coding regions of SEQ ID NO:1; and
- d) a genomic polynucleotide sequence having at least 95% identity to coding regions of SEQ ID NO: 1 over the entire coding regions of SEQ ID NO:1.

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17. An intron obtained from a genomic polynucleotide sequence selected from the group consisting of:

- a) a genomic polynucleotide sequence having at least 70% identity to coding regions of SEQ ID NO: 3 over the entire coding regions of SEQ ID NO:3;

b) a genomic polynucleotide sequence having at least 80% identity to coding regions of SEQ ID NO: 3 over the entire coding regions of SEQ ID NO:3;

c) a genomic polynucleotide sequence having at least 90% identity to coding regions of SEQ ID NO: 3 over the entire coding regions of SEQ ID NO:3; and

5 d) a genomic polynucleotide sequence having at least 95% identity to coding regions of SEQ ID NO: 3 over the entire coding regions of SEQ ID NO:3.

18. An intron obtained from a genomic polynucleotide sequence selected from the group consisting of:

10 a) a genomic polynucleotide sequence having at least 70% identity to coding regions of SEQ ID NO:23 over the entire coding regions of SEQ ID NO:23;

b) a genomic polynucleotide sequence having at least 80% identity to coding regions of SEQ ID NO:23 over the entire coding regions of SEQ ID NO:23;

c) a genomic polynucleotide sequence having at least 90% identity to coding regions of SEQ ID NO:23 over the entire coding regions of SEQ ID NO:23; and

15 d) a genomic polynucleotide sequence having at least 95% identity to coding regions of SEQ ID NO:23 over the entire coding regions of SEQ ID NO:23.

19. An intron obtained from a genomic polynucleotide sequence selected from the group consisting of:

20 a) a genomic polynucleotide sequence having at least 70% identity to coding regions of SEQ ID NO:27 over the entire coding regions of SEQ ID NO:27;

b) a genomic polynucleotide sequence having at least 80% identity to coding regions of SEQ ID NO:27 over the entire coding regions of SEQ ID NO:27;

c) a genomic polynucleotide sequence having at least 90% identity to coding regions of SEQ ID NO:27 over the entire coding regions of SEQ ID NO:27; and

d) a genomic polynucleotide sequence having at least 95% identity to coding regions of SEQ ID NO:27 over the entire coding regions of SEQ ID NO:27.

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20. A recombinant DNA construct comprising at least one of the polynucleotide sequences of Claims 1-19.

21. The recombinant DNA construct according to Claim 20, wherein said
10 polynucleotide sequence is an intron sequence.

22. The recombinant DNA construct according to Claim 21, wherein said intron sequence is in an orientation selected from the group consisting of sense and antisense.

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23. A plant cell comprising the DNA construct of 20.

24. A plant comprising the cell of Claim 24.

20 25. A method of modifying the fatty acid composition in a plant cell, said method comprising:

transforming a plant cell with the construct of Claim 21 and,
growing said cell under conditions wherein transcription of said polynucleotide sequence is initiated,

25 whereby said fatty acid composition of said cell is modified.

26. The method according to Claim 25, wherein said modification is selected from the group consisting of an increase in oleic acid, a decrease in linolenic acid and a decrease in linoleic acid.

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27. The method according to Claim 25, wherein said polynucleotide sequence is an intron sequence.

28. The method according to Claim 27, wherein said intron sequence is in an orientation selected from the group consisting of sense and antisense.

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29. A plant cell produced by the method of claim 25.

30. A method of inhibiting gene expression in a plant cell, comprising the steps of:
transforming a plant cell with a DNA construct comprising a non-coding region of a gene to be inhibited positioned in a sense orientation; and
growing said cell under conditions wherein transcription of said non-coding region is initiated, whereby said expression of said gene is inhibited.

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31. The method according to claim 30 wherein said non-coding region is selected from the group consisting of an intron, a promoter region, a 5' untranslated region and portions of such sequences.

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32. The method according to claim 30 wherein said non-coding region is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:24, SEQ ID NO:4, SEQ ID NO:5, SEQ ID

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NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28 and SEQ ID NO:29.

33. The method according to claim 30 wherein said gene encodes desaturase.

34. A method of inhibiting desaturase expression in a plant cell, comprising the steps of:
transforming a plant cell with a DNA construct comprising a non-coding region of a gene
encoding desaturase positioned in an antisense orientation; and
growing said cell under conditions wherein transcription of said non-coding region is
initiated; whereby said expression of said desaturase is inhibited.

35. The method according to claim 34 wherein said non-coding region is selected from
the group consisting of an intron, a promoter region, a 5' untranslated region and portions of such
sequences.

36. The method according to claim 34 wherein said non-coding region is selected from
the group consisting of SEQ ID NO:2, SEQ ID NO:24, SEQ ID NO:4, SEQ ID NO:5, SEQ ID
NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28 and SEQ ID
NO:29.

37. A plant cell produced according to the method of claim 34.

38. The plant cell according to claim 37 wherein said cell includes an oil composition
comprising at least about 80 - 85% oleic acid, no more than about 1 - 2% linoleic acid and no more
than about 1-3% linolenic acid.

39. The plant cell according to claim 37 wherein said cell includes an oil composition comprising at least about 50 - 75% oleic acid, no more than about 10 - 30% linoleic acid and no more than about 1-3% linolenic acid.

5 40. A method of modifying fatty acid composition in a plant cell, comprising the steps of:

transforming a plant cell with a DNA construct comprising a non-coding region of a gene encoding desaturase positioned in a sense or an antisense orientation; and

10 growing said cell under conditions wherein transcription of said non-coding region is initiated, whereby said expression of said desaturase is inhibited.

41. The method according to claim 40 wherein said non-coding region is selected from the group consisting of an intron, a promoter region, a 5' untranslated region and portions of such
15 sequences.

42. The method according to claim 41 wherein said non-coding region is selected from the group consisting of SEQ ID NO:2; SEQ ID NO:24, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:28 and SEQ ID
20 NO:29.

43. A plant cell produced according to the method of claim 40.

44. The plant cell according to claim 43 wherein said cell includes an oil composition comprising at least about 80 - 85% oleic acid, no more than about 1 - 2% linoleic acid and no more than about 1-3% linolenic acid.

5 45. The plant cell according to claim 43 wherein said cell includes an oil composition comprising at least about 50 - 75% oleic acid, no more than about 10 - 30% linoleic acid and no more than about 1-3% linolenic acid.

46. A method of inhibiting desaturase expression in a plant cell, comprising the steps of:
10 transforming a plant cell with a DNA construct comprising a nucleic acid sequence capable of binding to or cleaving a non-coding region of a gene encoding desaturase; and growing said cell under conditions wherein transcription of said nucleic acid sequence is initiated, whereby said expression of said desaturase is inhibited.

15 47. A plant cell produced according to the method of claim 46.

48. A oil seed composition comprising:
at least about 50 - 75% oleic acid, no more than about 10 - 30% linoleic acid and no more than about 1-3% linolenic acid.

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ABSTRACT